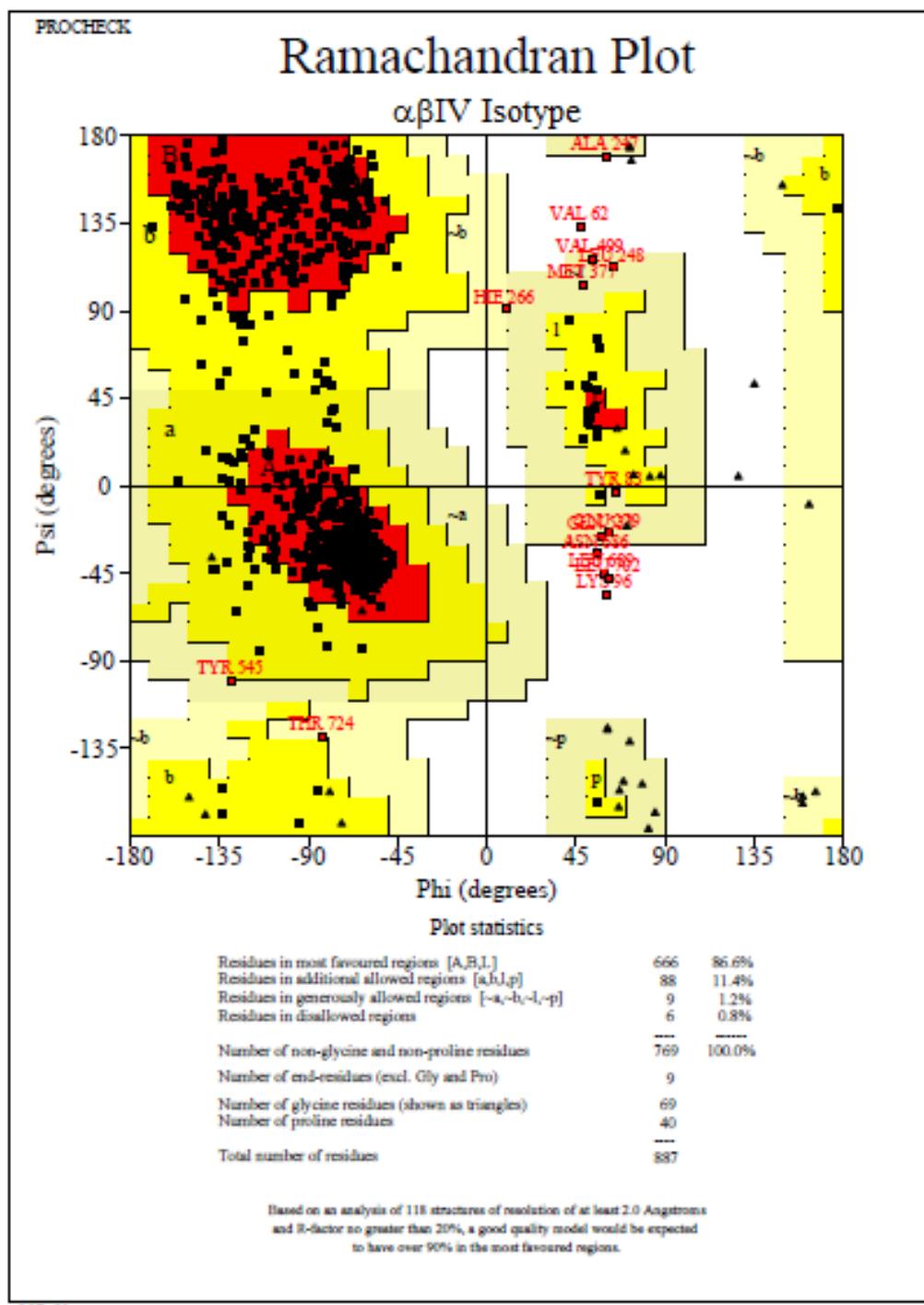
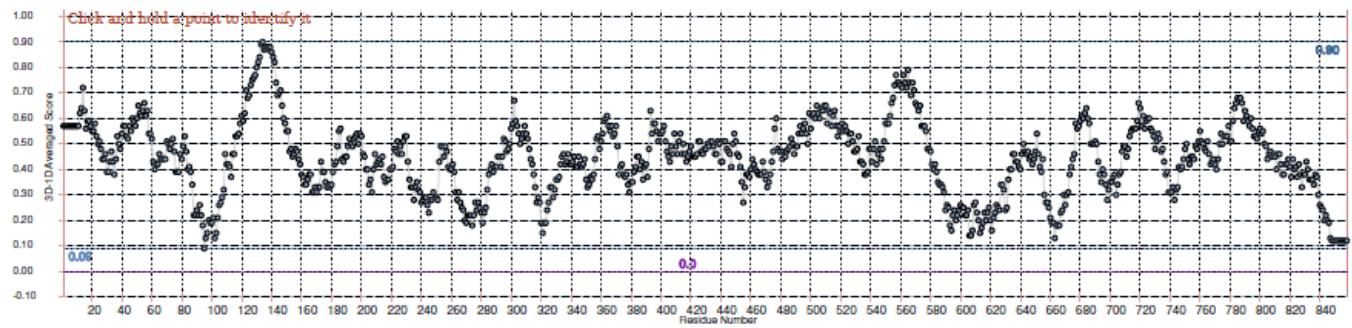


S4 Fig.



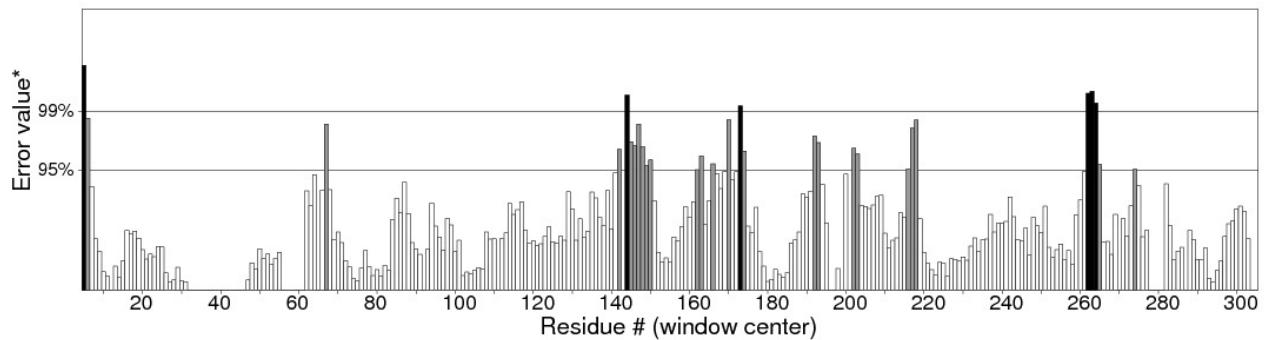
(A)

Verify-3D graph of $\alpha\beta$ IV Isotype



(B)

Program: ERRAT2
 File: /var/www/SAVES/Jobs/7149809//errat.pdb
 Chain#:1
 Overall quality factor**: 89.846



*On the error axis, two lines are drawn to indicate the confidence with which it is possible to reject regions that exceed that error value.

**Expressed as the percentage of the protein for which the calculated error value falls below the 95% rejection limit. Good high resolution structures generally produce values around 95% or higher. For lower resolutions (2.5 to 3 \AA) the average overall quality factor is around 91%.

(C)